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RAW SEQUENCE LISTING DATE: 01/14/2002 PATENT APPLICATION: US/10/018,706 TIME: 07:30:53
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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01142002\J018706.raw

```
Does Not Comply
      4 <110> APPLICANT: Thonnard, Joelle
                                                                         Corrected Diskette Needec
      6 <120> TITLE OF INVENTION: Cloning of BASB110 Antigen From
              Moraxella (Branhamella) Catarrhalis
     10 <130> FILE REFERENCE: BM45394
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/018,706
C--> 12 <141> CURRENT FILING DATE: 2001-12-13
     12 <150> PRIOR APPLICATION NUMBER: 9915031.0
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     15 <150> PRIOR APPLICATION NUMBER: PCT/EP00/05854
     16 <151> PRIOR FILING DATE: 2000-06-23
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     30 agtacctcag gttcgggcag tcatcgtact tcaggttcag gtggtttggc aataqqttca
                                                                               180
     31 caggttatca cggacagtca gggcgtacca aatcgctatc aggtgaagca gggcgatact
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     32 gtcagtaaga ttgctcagcg ttatggatta aattggcqtg agattggaca cattaataat
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     33 ctaaatagca gttatacgat ttatacaggt caatggctga ctttatggtc aggtgatctc
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     34 aaggtgegtg agegtagtat cagetetggt gtgaatacag etcaeacace ttegeetgtg
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     35 geggtteagt caageagace accagtacag cageateetg cegtacaaaa acceaegeea
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     36 cctgttgttg tggtaaaaaa acccacaccg actccgcctg tggttcagca gccagcacca
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     37 gttgccccac cagtgacaga agcaccattt gccacgggta gctcaggggt gatgcaattt
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     38 cgctatcctg ttggtgcgac caatccagtg gttcgacgct ttggtacggc gacagtggcc
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     39 ggctcaactg ttaccagtaa tggcatgtgg ttttctggac gagatggcga tttaattaac
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     40 gccagtaatg caggcacagt cattcaagct gatcacaata tggacggggc gagtattgtg
                                                                               780
     41 attcagcata ccaatggatt tgtttcaagc tatatccata ttaaggacgc tcaagttaaa
                                                                               840
     42 acaggegata eggtgegtae eggteagegt attgeaagea tgaaaaatea geeaageggt
                                                                               900
     43 geggeactat tigaatitag aatitetaga aatggegigt aigtigatee aitgaeagta
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     47 <211> LENGTH: 322
     48 <212> TYPE: PRT
     49 <213> ORGANISM: Moraxella catarrhalis
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    54 Arg Leu Gly Leu Ile Phe Gly Val Ile Thr Thr Cys Ile Leu Ala Gly
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    56 Cys Ala Ser Lys Pro Thr Tyr Asn Ser Thr Ser Gly Ser Gly Ser His
                                    40
    58 Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Ile Thr
    59
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60 Asp Ser Gln Gly Val Pro Asn Arg Tyr Gln Val Lys Gln Gly Asp Thr
62 Val Ser Lys Ile Ala Gln Arg Tyr Gly Leu Asn Trp Arg Glu Ile Gly
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64 His Ile Asn Asn Leu Asn Ser Ser Tyr Thr Ile Tyr Thr Gly Gln Trp
65
               100
                                   105
66 Leu Thr Leu Trp Ser Gly Asp Leu Lys Val Arg Glu Arg Ser Ile Ser
                               120
68 Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser
       130
                           135
                                               140
70 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro
                       150
                                           155
72 Pro Val Val Val Lys Lys Pro Thr Pro Thr Pro Pro Val Val Gln
                   165
                                       170
74 Gln Pro Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Phe Ala Thr
               180
                                   185
76 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn
           195
                               200
78 Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val
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                                               220
80 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn
                       230
                                           235
82 Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly
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                                       250
84 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile
               260
                                   265
86 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly
           275
                               280
88 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe
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91 305
92 Leu Lys
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105 gtcagtaaga ttgctcagcg ttatggatta aattggcgtg agattggaca cattaataat
                                                                           300
106 ctaaatagcg gttatacgat ttatacaggt caatggctga ctttatggtc aggtgatctc
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107 aaggtgcgtg agcgtagtat cagctctggt gtgaatacag ctcacacacc ttcgcctgtg
                                                                           420
108 geggtteagt caageagace accagtacag cageatectg cegtacaaaa acceaegeea
                                                                           480
109 cctgttgttg tggtaaaaaa acccacaccg actccgcctg tggttcagca gccagcacca
                                                                           540
                                                                           600
110 gttqccccac caqtqacaqa aqcaccattt qccacqqqta qctcaqqqqt qatqcaattt
111 cgctatcctg ttggtgcgac caatccagtg gttcgacgct ttggtacggc gacagtggcc
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114 attcagcata ccaatggatt tgtttcaagc tatatccata ttaaggacgc tcaagttaaa 115 acaggcgata cggtgcgtac cggtcagcgt attgcaagca tgaaaaatca gccaagcggt 116 gcggcactat ttgaatttag aatttctaga aatggcgtgt atgttgatcc attgacagta 117 cttaaa 119 <2110 > SEO ID NO: 4 120 <211> LENGTH: 322 121 <212> TYPE: PRT 122 <213> ORGANISM: Moraxella catarrhalis 124 <400> SEOUENCE: 4 125 Met Thr Val Thr Ile Ala Ile Asn Ser Gln Asn Gln Lys Pro Ile Lys 126 1 5 10 15 127 Arg Leu Gly Leu Ile Phe Gly Val Ile Thr Thr Cys Ile Leu Ala Gly 128 20 125 129 Cys Ala Ser Lys Pro Thr Tyr Asn Ser Thr Ser Gly Ser Gly Ser His 130 35 40 45 131 Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Ile Thr 134 65 70 80 135 Val Ser Lys Ile Ala Gln Arg Tyr Gly Leu Asn Trp Arg Glu Ile Gly 136 85 90 95 137 His Ile Asn Asn Leu Asn Ser Gly Tyr Thr Ile Tyr Thr Gly Gln Trp 138 100 115 120 141 Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser 142 130 135 143 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro 144 145 150 150 145 Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Pro Val Val Gln 146 165 170 175 147 Gln Pro Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Phe Ala Thr 148 180 180 185 190 149 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Cly Ala Thr Asn 150 195 200 151 Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val 152 100 195 200 153 Thr Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly 154 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 155 Ala Ser Arg Ile Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly 156 245 250 256 157 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 158 260 265 270 159 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly 160 275 280 161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Asp Leu Ile Asn 162 290 295 300																attaac attgtg	720 780
115 acaggigata cggtigitac cggtiagigat attiginal attigina	gecagtaatg caggeacagt catteaaget gateacaata tggaegggge gagtattgtg																
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117 cttaaa 119 <210> SEQ ID NO: 4 120 <211> LENGTH: 322 121 <212> TYPE: PRT 122 <213> ORGANISM: Moraxella catarrhalis 124 <400> SEQUENCE: 4 125 Met Thr Val Thr Ile Ala Ile Asn Ser Gln Asn Gln Lys Pro Ile Lys 126 1 5 10 15 127 Arg Leu Gly Leu Ile Phe Gly Val Ile Thr Thr Cys Ile Leu Ala Gly 128 20 25 30 129 Cys Ala Ser Lys Pro Thr Tyr Asn Ser Thr Ser Gly Ser Gly Ser His 130 35 40 45 131 Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Ile Thr 132 50 60 133 Asp Ser Gln Gly Val Pro Asn Arg Tyr Gln Val Lys Gln Gly Asp Thr 134 65 70 75 80 135 80 136 85 80 137 His Ile Asn Asn Leu Asn Ser Gly Tyr Thr Ile Tyr Thr Gly Gln Trp 138 100 105 110 139 Leu Thr Leu Trp Ser Gly Asp Leu Lys Val Arg Glu Arg Ser Ile Ser 140 115 120 141 Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser 142 130 135 140 143 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro 144 145 150 165 170 144 145 165 170 145 180 180 190 190 190 157 190 190 190 158 190 190 190 159 190 190 190 159 190 190 190 150 190 190 150 190 151 Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Pro Val Gly Ala Thr 148 180 190 200 205 151 Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val 152 210 205 153 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn 154 225 230 235 240 155 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 158 260 270 159 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly 160 175 181 191 194 181 195 194 181 195 194 181 195 195 150																	
119																	
120											700						
121																	
122																	
124																	
125 Met Thr Val Thr The Ala The Ala The Ala The Ala The Ala The Ala The The The Thr Cys The Leu Ala Gly Cys Arg Leu Gly Leu Trp Ser Gly Ser																	
126						Ala	Tle	Agn	Ser	Gln	Agn	Gln	Lvc	Pro	Tle	T.vs	
127 Arg Leu Gly Leu Ile Phe Gly Val Ile Thr Thr Cys Ile Leu Ala Gly 20 25 30 30 30 31 31 32 35 40 40 45 45 31 Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gly Ser Gly Ser His 35 35 36 35 36 35 36 36		1111	·	1111		mu	110	non	DCI		non	OIII	цуз	110		БуЗ	
128		T.eu	Glv	T.e.u		Pho	G1 v	Va l	Tla		Thr	Cve	Tle	T.011		Glv	
129 Cys		Dea	011		110	1 110	011	141		1111	1 111	Cys	110		mu	OLY	
130		Δla	Ser		Pro	Thr	Фυν	Δen		Thr	Sor	G1v	Sor		Sar	Uic	
131 Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Thr Thr 132 50 55 60 60 60 61 61 61 65 60 61 61 61 61 61 61 61		1114		цу	110	1111	-1-		DCI	1111	DCI	Ory		OLY	DCI	1113	
132		Thr		G1 _v	Sar	G1 57	G1 _v		λla	Tla	Clv	Cor		17 a 1	Tla	mhr.	
133			Der	GIY	Del	GIY		пец	AIU	TIC	GIY		GIII	val	116	1111	
134 65			Gln.	Gl v	Val	Dro		λνα	Тиг	Cln	Wa 1		Cln	C1 17	λαn	Thr	
135		Der	GIII	Gry	Val		non.	Arg	TYL	GIII		шyз	GIII	GIY	тэр		
136		Sar	T.v.c	τlΔ	λla		λκα	Пτεν	Clv	T Au		Trn	λνα	Clu	Tlo		
137	vai	DCI	цуз	110		GIII	nra	TYL	Gry		ASII	115	мту	GIU		GIY	
138	Hic	Tle	Δen	Δen	-	Δen	Sar	Glv	Тулт		ΤlΔ	Фτε	Thr	C1 v		Trn	
139 Leu Thr Leu Trp Ser Gly Asp Leu Lys Val Arg Glu Arg Ser Ile Ser 140	111.5	110	ASH		пси	поп	DCI	GLY		1111	116	TYL	T 111	_	GIII	тъ	
140 115 120 125 141 Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser 142 130 135 140 143 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro Ala Val Gln Lys Pro Thr Pro Thr Pro Thr Pro Thr Pro Val Val Gln 160 150 144 145 150 170 175 147 Gln Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Thr Pro Pro Val Val Gln 175 175 147 Gln Pro Ala Pro Val Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Pro Val Gly Ala Thr 190 149 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn 205 151 Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val 152 153 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn 240 155 220 153 Thr Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly 255 155 240 156 265 157 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 260 158 260 275 280 280 285 161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Ala Leu Phe	I.e.ii	Thr	T.011		Ser	Glv	Δen	T.Q11		Va 1	Δra	Glu	Δτα		τlα	Sor	
141 Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser 142 130 135 140 143 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro 155 160 144 145 150 155 155 146 145 150 155 160 145 Pro Val Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Thr Pro Val Val Gln 175 176 175 147 Gln Pro Ala Pro Val Ala Thr 185 180 185 190 149 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn 190 195 200 205 205 151 Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val 152 220 220 220 220 153 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn 230 235 240 155 Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly 255 255 157 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 260 265 270 159 150 265 270 285 160 275 280 285 Thr Val Ala Ala Leu Phe<	Lou			+	001		P		Lys	· u.	1119	Olu	-	OC1	110	Ser	
142 130 135 140 143 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro 144 145 145 150 150 155 160 144 145 140 Val Val Val Lys Lys Pro Thr Pro 155 160 160 145 Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Thr Pro Pro Val Val Gln 175 175 175 147 Gln Pro Ala Pro Val Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Phe Ala Thr 180 185 190 149 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn 195 200 205 151 Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val 220 205 153 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn 230 235 240 155 Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly 245 255 255 157 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 265 265 270 159 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly Asp Thr Val Arg Thr Gly 285 265 270 160 275 280 285 Thr Val Ala Ala Leu Phe	Ser	Glv		Asn	Thr	Δla	His		Pro	Ser	Pro.	Va 1		Va 1	Gln	Sor	
143 Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro 144 145	OCI		, u.	11511	1111	mu		1111	110	DCI	110		niu	Val	GIII	Ser	
144 145	Ser		Pro	Pro	Va 1	Gln		His	Pro	Δla	Va l		T.vc	Dro	Thr	Dro	
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146 Image: contract of the contr		Va 1	Va 1	Va 1	Va 1		Lvs	Pro	Thr	Pro		Pro	Pro	Va 1	Va l		
147 Gln Pro Ala Pro Val Ala Pro Val Thr Glu Ala Pro Phe Ala Thr Ala Thr Ala Thr Pro Val Gly Ala Thr Phe Arg Pro Val Ala Thr Asn Ala Gly Arg Phe Ala Thr Ala Thr Val Ala Gly Ser Thr Val Ala A		, , ,		, 41		_10	L ₁ U	110			1111	110	110	vul		OIII	
148 180 185 190 149 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn 150 195 200 205 151 Pro Val Val Arg Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val 152 210 215 220 153 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn 240 154 225 230 230 235 240 155 Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly 61y 255 157 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 255 158 260 265 270 159 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly 285 161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe	Gln	Pro	Δla	Pro		Ala	Pro	Pro	Val		Glu	Δla	Pro	Phe		Thr	
149 Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn 150											014				1114	- · · · ·	
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153 Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn 154 225			, 41			1		****			, u ı		011	OCL	1111	var .	
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156		Ser	Asn	Ala	Glv		Val	Tle	Gln	Ala		His	Asn	Met	Asn		
157 Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile 158 260 265 270 159 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly 160 275 280 285 161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe							,								_	011	
158 260 265 270 159 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly 280 285 161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe	Ala	Ser	Ile	Val		Gln	His	Thr	Asn		Phe	Va 1	Ser	Ser		T]e	
159 His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly 160 275 280 285 161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe										1					-1-		
160 275 280 285 161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe	His	Ile	Lys		Ala	Gln	Val	Lys		Glv	Asp	Thr	Val		Thr	Glv	
161 Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe				~ [1	F			5		<u>1</u>	•
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Output Set: N:\CRF3\01142002\J018706.raw

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VERIFICATION SUMMARY

DATE: 01/14/2002

PATENT APPLICATION: US/10/018,706 TIME: 07:30:54

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\01142002\J018706.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:171 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5